



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Collins, Mary  
Donaldson, Debra  
Fitz, Lori  
Neben, Tamlyn  
Whitters, Matthew  
Wood, Clive

(ii) TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.  
(B) STREET: 87 CambridgePark Drive  
(C) CITY: Cambridge  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brown, Scott A.  
(B) REGISTRATION NUMBER: 32,724  
(C) REFERENCE/DOCKET NUMBER: GI5268

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1525 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 256..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|   |     |
|---|-----|
| GAATTCGGCA CGAGGGAGAG GAGGAGGGAA AGATAGAAAG AGAGAGAGAA AGATTGCTTG | 60  |
| CTACCCCTGA ACAGTGACCT CTCTCAAGAC AGTGCTTTGC TCTTCACGTA TAAGGAAGGA | 120 |
| AAACAGTAGA GATTCAATTT AGTGTCTAAT GTGGAAAGGA GGACAAAGAG GTCTTGTGAT | 180 |
| AACTGCCTGT GATAATACAT TTCTTGAGAA ACCATATTAT TGAGTAGAGC TTTCAGCACA | 240 |
| CTAAATCCTG GAGAA ATG GCT TTT GTG CAT ATC AGA TGC TTG TGT TTC ATT  | 291 |
| Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile                   |     |
| 1 5 10  |     |
| CTT CTT TGT ACA ATA ACT GGC TAT TCT TTG GAG ATA AAA GTT AAT CCT   | 339 |
| Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro   |     |
| 15 20 25  |     |
| CCT CAG GAT TTT GAA ATA TTG GAT CCT GGA TTA CTT GGT TAT CTC TAT   | 387 |
| Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr   |     |
| 30 35 40  |     |
| TTG CAA TGG AAA CCT CCT GTG GTT ATA GAA AAA TTT AAG GGC TGT ACA   | 435 |
| Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr   |     |
| 45 50 55 60   |     |
| CTA GAA TAT GAG TTA AAA TAC CGA AAT GTT GAT AGC GAC AGC TGG AAG   | 483 |
| Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys   |     |
| 65 70 75  |     |
| ACT ATA ATT ACT AGG AAT CTA ATT TAC AAG GAT GGG TTT GAT CTT AAT   | 531 |
| Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn   |     |
| 80 85 90  |     |
| AAA GGC ATT GAA GGA AAG ATA CGT ACG CAT TTG TCA GAG CAT TGT ACA   | 579 |
| Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr   |     |
| 95 100 105  |     |
| AAT GGA TCA GAA GTA CAA AGT CCA TGG ATA GAA GCT TCT TAT GGG ATA   | 627 |
| Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile   |     |
| 110 115 120   |     |
| TCA GAT GAA GGA AGT TTG GAA ACT AAA ATT CAG GAC ATG AAG TGT ATA   | 675 |
| Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile   |     |
| 125 130 135 140   |     |
| TAT TAT AAC TGG CAG TAT TTG GTC TGC TCT TGG AAA CCT GGC AAG ACA   | 723 |

|  |      |
|--|------|
| Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr            |      |
| 145 150 155  |      |
| GTA TAT TCT GAT ACC AAC TAT ACC ATG TTT TTC TGG TAT GAG GGC TTG            | 771  |
| Val Tyr Ser Asp Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu            |      |
| 160 165 170  |      |
| GAT CAT GCC TTA CAG TGT GCT GAT TAC CTC CAG CAT GAT GAA AAA AAT            | 819  |
| Asp His Ala Leu Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn            |      |
| 175 180 185  |      |
| GTT GGA TGC AAA CTG TCC AAC TTG GAC TCA TCA GAC TAT AAA GAT TTT            | 867  |
| Val Gly Cys Lys Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe            |      |
| 190 195 200  |      |
| TTT ATC TGT GTT AAT GGA TCT TCA AAG TTG GAA CCC ATC AGA TCC AGC            | 915  |
| Phe Ile Cys Val Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser            |      |
| 205 210 215 220  |      |
| TAT ACA GTT TTT CAA CTT CAA AAT ATA GTT AAA CCA TTG CCA CCA GAA            | 963  |
| Tyr Thr Val Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu            |      |
| 225 230 235  |      |
| TTC CTT CAT ATT <del>ACC</del> GTG GAG AAT TCC ATT GAT ATT AGA ATG AAA TGG | 1011 |
| Phe Leu His Ile Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp            |      |
| 240 245 250  |      |
| AGC ACA CCT GGA GGA CCC ATT CCA CCA AGG TGT TAC ACT TAT GAA ATT            | 1059 |
| Ser Thr Pro Gly Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile            |      |
| 255 260 265  |      |
| GTG ATC CGA GAA GAC GAT ATT TCC TGG GAG TCT GCC ACA GAC AAA AAC            | 1107 |
| Val Ile Arg Glu Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn            |      |
| 270 275 280  |      |
| GAT ATG AAG TTG AAG AGG AGA GCA AAT GAA AGT GAA GAC CTA TGC TTT            | 1155 |
| Asp Met Lys Leu Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe            |      |
| 285 290 295 300  |      |
| TTT GTA AGA TGT AAG GTC AAT ATA TAT TGT GCA GAT GAT GGA ATT TGG            | 1203 |
| Phe Val Arg Cys Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp            |      |
| 305 310 315  |      |
| AGC GAA TGG AGT GAA GAG GAA TGT TGG GAA GGT TAC ACA GGG CCA GAC            | 1251 |
| Ser Glu Trp Ser Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp            |      |
| 320 325 330  |      |
| TCA AAG ATT ATT TTC ATA GTA CCA GTT TGT CTT TTC TTT ATA TTC CTT            | 1299 |
| Ser Lys Ile Ile Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu            |      |
| 335 340 345  |      |
| TTG TTA CTT CTT TGC CTT ATT GTG GAG AAG GAA GAA CCT GAA CCC ACA            | 1347 |
| Leu Leu Leu Leu Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr            |      |
| 350 355 360  |      |

TTG AGC CTC CAT GTG GAT CTG AAC AAA GAA GTG TGT GCT TAT GAA GAT 1395  
 Leu Ser Leu His Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp  
 365 370 375 380

ACC CTC TGT TAAACCACCA ATTTCTTGAC ATAGAGCCAG CCAGCAGGAG 1444  
 Thr Leu Cys

TCATATTAAA CTCAATTCTT CTTAAATTT CGAATACATC TTCTTGAAAA TCCAAAAAAA 1504  
 AAAAAAAAAA AAAAAGCTCGA G 1525

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Phe | Val | His | Ile | Arg | Cys | Leu | Cys | Phe | Ile | Leu | Leu | Cys | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Thr | Gly | Tyr | Ser | Leu | Glu | Ile | Lys | Val | Asn | Pro | Pro | Gln | Asp | Phe |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ile | Leu | Asp | Pro | Gly | Leu | Leu | Gly | Tyr | Leu | Tyr | Leu | Gln | Trp | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Pro | Val | Val | Ile | Glu | Lys | Phe | Lys | Gly | Cys | Thr | Leu | Glu | Tyr | Glu |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Lys | Tyr | Arg | Asn | Val | Asp | Ser | Asp | Ser | Trp | Lys | Thr | Ile | Ile | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Asn | Leu | Ile | Tyr | Lys | Asp | Gly | Phe | Asp | Leu | Asn | Lys | Gly | Ile | Glu |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Gly | Lys | Ile | Arg | Thr | His | Leu | Ser | Glu | His | Cys | Thr | Asn | Gly | Ser | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Gln | Ser | Pro | Trp | Ile | Glu | Ala | Ser | Tyr | Gly | Ile | Ser | Asp | Glu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Leu | Glu | Thr | Lys | Ile | Gln | Asp | Met | Lys | Cys | Ile | Tyr | Tyr | Asn | Trp |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Gln | Tyr | Leu | Val | Cys | Ser | Trp | Lys | Pro | Gly | Lys | Thr | Val | Tyr | Ser | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Asn | Tyr | Thr | Met | Phe | Phe | Trp | Tyr | Glu | Gly | Leu | Asp | His | Ala | Leu |

|   |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|
|   | 165 |     | 170 |     | 175 |
| Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn Val Gly Cys Lys |     |     |     |     |     |
|   | 180 |     | 185 |     | 190 |
| Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe Phe Ile Cys Val |     |     |     |     |     |
|   | 195 |     | 200 |     | 205 |
| Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser Tyr Thr Val Phe |     |     |     |     |     |
|   | 210 |     | 215 |     | 220 |
| Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu Phe Leu His Ile |     |     |     |     |     |
|   | 225 |     | 230 |     | 240 |
| Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp Ser Thr Pro Gly |     |     |     |     |     |
|   |     | 245 |     | 250 | 255 |
| Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile Val Ile Arg Glu |     |     |     |     |     |
|   | 260 |     | 265 |     | 270 |
| Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn Asp Met Lys Leu |     |     |     |     |     |
|   | 275 |     | 280 |     | 285 |
| Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe Phe Val Arg Cys |     |     |     |     |     |
|   | 290 |     | 295 |     | 300 |
| Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp Ser Glu Trp Ser |     |     |     |     |     |
|   | 305 |     | 310 |     | 320 |
| Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp Ser Lys Ile Ile |     |     |     |     |     |
|   |     | 325 |     | 330 | 335 |
| Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu Leu Leu Leu Leu |     |     |     |     |     |
|   | 340 |     | 345 |     | 350 |
| Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr Leu Ser Leu His |     |     |     |     |     |
|   | 355 |     | 360 |     | 365 |
| Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp Thr Leu Cys     |     |     |     |     |     |
|   | 370 |     | 375 |     | 380 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 103..1245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|   |     |
|---|-----|
| GGATCCGCGC GGATGAAGGC TATTTGAAGT CGCCATAACC TGGTCAGAAG TGTGCCTGTC | 60  |
| GGCGGGGAGA GAGGCAATAT CAAGGTTTTA AATCTCGGAG AA ATG GCT TTC GTT    | 114 |
| Met Ala Phe Val   |     |
| 1   |     |
| TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA TTT   | 162 |
| Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe   |     |
| 5 10 15 20  |     |
| GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT CAG   | 210 |
| Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln   |     |
| 25 30 35  |     |
| GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG CAA   | 258 |
| Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln   |     |
| 40 45 50  |     |
| TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG GAA   | 306 |
| Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu   |     |
| 55 60 65  |     |
| TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC ATC   | 354 |
| Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile   |     |
| 70 75 80  |     |
| ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG GGC   | 402 |
| Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly   |     |
| 85 90 95 100  |     |
| ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT GGA   | 450 |
| Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly   |     |
| 105 110 115   |     |
| TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA CCA   | 498 |
| Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro   |     |
| 120 125 130   |     |
| CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT TAC   | 546 |
| Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr Tyr   |     |
| 135 140 145   |     |
| AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA CTT   | 594 |
| Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val Leu   |     |
| 150 155 160   |     |
| CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT CAT   | 642 |
| Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His   |     |
| 165 170 175 180   |     |

|   |      |
|---|------|
| GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA GGA   | 690  |
| Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly   |      |
| 185 190 195   |      |
| TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT ATT   | 738  |
| Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile   |      |
| 200 205 210   |      |
| TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT TTC   | 786  |
| Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe   |      |
| 215 220 225   |      |
| ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT CTT   | 834  |
| Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr Leu   |      |
| 230 235 240   |      |
| ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC ATA   | 882  |
| Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile   |      |
| 245 250 255 260   |      |
| CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG ATC   | 930  |
| Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile   |      |
| 265 270 275   |      |
| AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA ACA   | 978  |
| Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu Thr   |      |
| 280 285 290   |      |
| TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA GTA   | 1026 |
| Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val Val   |      |
| 295 300 305   |      |
| AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT GAG   | 1074 |
| Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu   |      |
| 310 315 320   |      |
| TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA ACT   | 1122 |
| Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr   |      |
| 325 330 335 340   |      |
| TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT ATA   | 1170 |
| Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val Ile   |      |
| 345 350 355   |      |
| TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA ATG   | 1218 |
| Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys Met   |      |
| 360 365 370   |      |
| ATT CCA GAA TTT TTC TGT GAT ACA TGA AGACTTTCCA TATCAAGAGA         | 1265 |
| Ile Pro Glu Phe Phe Cys Asp Thr *                                 |      |
| 375 380   |      |
| CATGGTATTG ACTCAACAGT TTCCAGTCAT GGCCAAATGT TCAATATGAG TCTCAATAAA | 1325 |
| CTGAATTTTT CTTGCGAAAA AAAAAAAAAA AAATCCGCGG ATCC                  | 1369 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile  
1 5 10 15  
Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val  
20 25 30  
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
35 40 45  
Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu  
50 55 60  
Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
65 70 75 80  
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
85 90 95  
Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
100 105 110  
Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr  
115 120 125  
Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp  
130 135 140  
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
145 150 155 160  
Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu  
165 170 175  
Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly  
180 185 190  
Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys  
195 200 205  
Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg  
210 215 220  
Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro



|   |     |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|-----|
| 225   |     | 230 |     | 235 |     | 240 |
| Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu |     |     |     |     |     |     |
|   | 245 |     |     | 250 |     | 255 |
| Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr |     |     |     |     |     |     |
|   | 260 |     | 265 |     |     | 270 |
| Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val |     |     |     |     |     |     |
|   | 275 |     | 280 |     |     | 285 |
| Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu |     |     |     |     |     |     |
|   | 290 |     | 295 |     | 300 |     |
| Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly |     |     |     |     |     |     |
| 305   |     | 310 |     | 315 |     | 320 |
| Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu |     |     |     |     |     |     |
|   | 325 |     | 330 |     |     | 335 |
| Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu |     |     |     |     |     |     |
|   | 340 |     | 345 |     |     | 350 |
| Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr |     |     |     |     |     |     |
|   | 355 |     | 360 |     |     | 365 |
| Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr *               |     |     |     |     |     |     |
|   | 370 |     | 375 |     | 380 |     |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

KSRCTCCABK CRCTCCA

17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAGTTAAAC CATTGCCACC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCCATTCGC TCCAAATTCC

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGTCTATCTT ACTTTTACTC G

21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATCTGAGCA ATAAATATTC AC

22